



Blast 2 Sequences results

PubMed

Entrez

BLAST

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Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.000** wordsize: **3** Filter View option **Standard**

Masking character option **X** for protein, **n** for nucleotide Masking color option **Black**

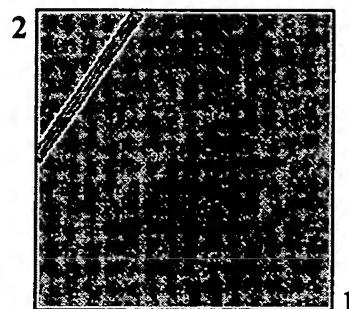
Show CDS translation **Align**

Sequence 1: lcl|1_seq_WNV20

Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_JEV

Length = 111 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 97.8 bits (242), Expect = 2e-19
 Identities = 42/54 (77%), Positives = 51/54 (94%), Gaps = 0/54 (0%)

Query 1 TPVGRLVTVPFVSVATANSKVLIELEPPFSDSYIVVGRGEQQINHHWHKSGSS 54
 TPVGRLVTVPFV+ ++ANSKVL+E+EPPF DSYIVVG G++QINHHWHK+GS+
 Sbjct 58 TPVGRLVTVPFVATSSANSKVLVEMEPPFGDSYIVVGMGDKQINHHWHKAGST 111

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
 0.322 0.137 0.417

Gapped
 Lambda K H
 0.267 0.0410 0.140



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Masking character option **X** for protein, **n** for nucleotide Masking color option **Black**

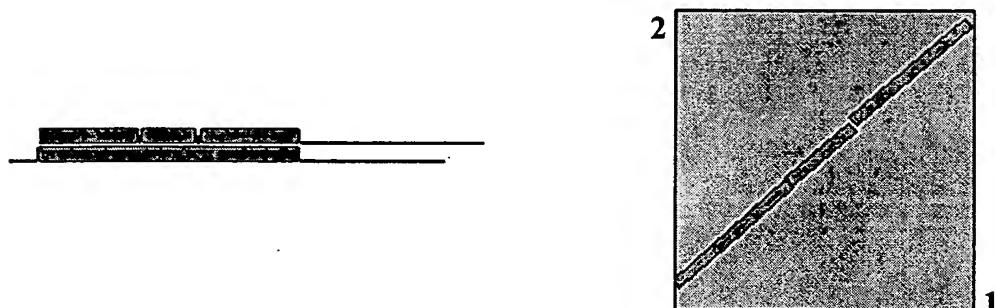
Show CDS translation **Align**

Sequence 1: lcl|1_seq_Dengue

Length = 94 (1 .. 160)

Sequence 2: lcl|2_seq_JEV

Length = 111 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 91.3 bits (225), Expect = 1e-17
 Identities = 41/96 (42%), Positives = 61/96 (63%), Gaps = 3/96 (3%)

Query 1	MCSGKFSIDKEMAETQHGTTVVKVYEGAGAPCKVPI-EIRDVNKEKVVGRIISSTPL--	57
	MC+ KFS K A+T HGT V+++ Y G+ PCK+PI + +N VGR+++ P	
Sbjct 12	MCTEKFSFAKNPADTGHGTVVIELSYSGSDGPCKIPIVSVASLNDMTPVGRLLTVNPFA	71
Query 58	AENTNSVTNIELEPPFGDSYIVIGVGNALTLHWFR	93
	+ NS +E+EPPFGDSYIV+G+G+ + HW +	
Sbjct 72	TSSANSKVLVEMEPPFGDSYIVVGMGDKQINHHWHK	107

CPU time: 0.01 user secs. 0.00 sys. secs 0.01 total secs.

Lambda	K	H
0.315	0.133	0.390



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Matrix **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter View option **Standard**

Masking character option **X** for protein, **n** for nucleotide Masking color option **Black**

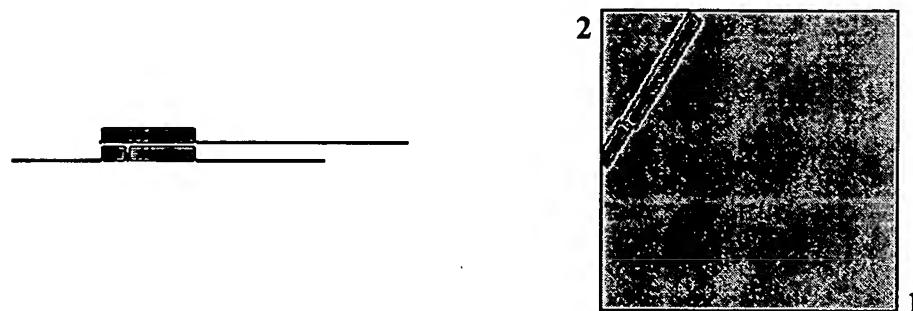
Show CDS translation **Align**

Sequence 1: lcl|1_seq_WNV20

Length = 154 (1 .. 160)

Sequence 2: lcl|2_seq_dengue

Length = 94 (1 .. 160)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 47.4 bits (111), Expect = 2e-04
 Identities = 22/48 (45%), Positives = 28/48 (58%), Gaps = 2/48 (4%)

Query 3 VGRLVTVNPFVSVATANSKVLIELEPPFSDSYIVVGRGEQQINHHWHK 50
 VGR+++ P NS IELEPPF DSYIV+G G + HW +
 Sbjct 48 VGRIISSTPLAE--NTNSVTNIELEPPFGDSYIVIGVGNSALTLHWFR 93

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
 0.322 0.137 0.417

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 104
Number of extensions: 63
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 (7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.9 bits)
S2: 72 (32.3 bits)

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 90
Number of extensions: 42
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 94
Length of database: 1,357,962,904
Length adjustment: 69
Effective length of query: 25
Effective length of database: 1,357,962,835
Effective search space: 33949070875
Effective search space used: 33949070875
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (22.0 bits)
S2: 71 (32.0 bits)

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 135
Number of extensions: 65
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 154
Length of database: 1,340,658,132
Length adjustment: 121
Effective length of query: 33
Effective length of database: 1,340,658,011
Effective search space: 44241714363
Effective search space used: 44241714363
Neighboring words threshold: 9
X1: 16 (7.4 bits)
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